

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/620,795A  
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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/620,795A

DATE: 07/19/2006

TIME: 09:21:32

Input Set : F:\UTSK352.APP.txt

Output Set: N:\CRF4\07192006\J620795A.raw

3 <110> APPLICANT: BARBOUR, ALAN G.  
 4 CARTER, CAROL  
 6 <120> TITLE OF INVENTION: A DIAGNOSTIC TEST FOR INFECTION WITH A SPIROCHETE BORNE  
 7 BY AMBLYOMMA AMERICANUM  
 9 <130> FILE REFERENCE: UTSK:352USC1  
 11 <140> CURRENT APPLICATION NUMBER: 10/620,795A  
 12 <141> CURRENT FILING DATE: 2003-07-14  
 14 <150> PRIOR APPLICATION NUMBER: 08/437,013  
 15 <151> PRIOR FILING DATE: 1995-05-08  
 17 <150> PRIOR APPLICATION NUMBER: 09/275,506  
 18 <151> PRIOR FILING DATE: 1999-03-24  
 20 <160> NUMBER OF SEQ ID NOS: 38  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 641  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 31 Primer  
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 35 attaacagag ttgctgatca ggctcaatac aaccagatgc atatgttatac taacaaatca 120  
 36 tctgctcaaa atgtaaaaac tgctgaagag cttggaatgc aacctgcaa aattaataca 180  
 37 ccagcatcac taactggagc acaagcttca tggacattga gagttcagg aggtgcaa 240  
 38 cagatgaag caattgctgt taatatttc tcaactaatg ttgcaaattt ttttgtgaa 300  
 39 gaagggttcc aaggcgctcc agctcaagag ggtgcacaac aggagggagt tcaaccagct 360  
 40 ccagctcaag gtgggattag ctctccaatt aatgttacaa ctgctatttg tgctaatgca 420  
 41 tcgcttacaa agattgaaga tgcttattga atggtaactg atcaaagagc aaatcttgg 480  
 42 gcttccaaa atagacttga gtctgttaaa gctgcacag attatgttat tgaaaactta 540  
 43 aaagcgtctt atgctcaa ataaagatgca ataatgacag atgaaatttg agcatctaca 600  
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 49 <212> TYPE: PRT  
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 52 <220> FEATURE:  
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 57 Thr Tyr Ser Asp Ala Asp Arg Gly Ser Ile Gln Ile Glu Ile Glu Gln  
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63 Met His Met Leu Ser Asn Lys Ser Ser Ala Gln Asn Val Lys Thr Ala
64          35          40          45
66 Glu Glu Leu Gly Met Gln Pro Ala Lys Ile Asn Thr Pro Ala Ser Leu
67          50          55          60
69 Thr Gly Ala Gln Ala Ser Trp Thr Leu Arg Val Gln Val Gly Ala Asn
70  65          70          75          80
72 Gln Asp Glu Ala Ile Ala Val Asn Ile Phe Ser Thr Asn Val Ala Asn
73          85          90          95
75 Leu Phe Gly Glu Gly Val Gln Ala Ala Pro Ala Gln Glu Gly Ala
76          100         105         110
78 Gln Gln Glu Gly Val Gln Pro Ala Pro Ala Gln Gly Gly Ile Ser Ser
79          115         120         125
81 Pro Ile Asn Val Thr Thr Ala Ile Asp Ala Asn Ala Ser Leu Thr Lys
82          130         135         140
84 Ile Glu Asp Ala Ile Arg Met Val Thr Asp Gln Arg Ala Asn Leu Gly
85  145         150         155         160
87 Ala Phe Gln Asn Arg Leu Glu Ser Val Lys Ala Ser Thr Asp Tyr Ala
88          165         170         175
90 Ile Glu Asn Leu Lys Ala Ser Tyr Ala Gln Ile Lys Asp Ala Ile Met
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96 Ala Met Ala Met Ile
97          210
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101 <211> LENGTH: 1336
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111 cgggtgagta acgcgtggat aatctgccta cgagatgggg ataactatta gaaataatag 120
112 ctaataccga ataaagtcaa ttgagttgtt agttgtgaa aggaagcctt taaagcttcg 180
113 ctgttagatg agtctcgctc ttattagcta gttgttaggg taagagccta ccaaggctat 240
114 gataagtaac cggcctgaga gggtgatcg tcacactgga actgagatac ggtccagact 300
115 cctacgggag gcagcagcta agaatcttcc gcaatggcg aaagcctgac ggagcgacac 360
116 tgcgtgaacg aagaaggctg aaagattgt aagtctttt ataaatgagg aataagctt 420
117 gtaggaaatg acaagggtat gacgttaatt tatgataaag ccccggtctaa ttacgtgcc 480
118 gcagccgcgg taatacgtaa ggggcccggc ttgttccggta tcattggcg taaagggtga 540
119 gtaggcggat atgtaagtct atgtgtaaaa taccacggct caactgtgga actatgctag 600
120 aaactgcattt actagagtct gataggggaa gttagaattc ctgggtgtaa ggtggatct 660
121 gttgatatac ggaagaatac cagaggcgaa agcgaacctc taggtcaaga ctgacgctga 720
122 gtcacgaaag cgtagggagc aaacaggatt agataccctg gtatgtctacg ctgtaaacg 780
123 tgcacacttg gtgttaatcg aaaggtagt accgaagctt acgtgttaag tgtgcccct 840
124 ggggagttatg ctcgcagag tgaaactcaa aggaattgac gggggcccg acaagcggtg 900
125 gagcatgtgg tttaattcga tgatacgcga ggaaccttac cagggcttga catatacagg 960

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126 atatagttag agataactac tctccgtttg gggctgtat acaggtgctg catgggtgtc 1020  
 127 gtcagctcggt gctgtgaggt gttgggttaa gtcccgcaac gagcgcaacc cttgttgtct 1080  
 128 gtaccagca tgtaaaagatg gggactcaga cgagactgcc ggtgataagc cggaggaagg 1140  
 129 tgaggatgac gtcaaattcat catggccctt atgtcctggg ctacacacgt gctacaatgg 1200  
 130 cctgtacaaa gcgatgcgaa acagtgtatgt gaagcaaaac gcataaaagca ggtctcagtc 1260  
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 142 Primer  
 144 <400> SEQUENCE: 4  
 145 aactgctgaa gagcttgaa tgcaaccctgc aaaaattaat acaccagcat cactaactgg 60  
 146 accacaagct tcatggacat tgagagttca ggtaggtgca aatcaggatg aagcaattgc 120  
 147 tttaatatt ttctcaacta atgttgaaa tctttttgtt ggagaagggtt ttcaagcggc 180  
 148 tccagctcaa gagggtgcac aacaggagg agttcaacca gctccagctc aaggtggat 240  
 149 tagctctcca attaatgtta caactgttat tgatgctaatt gcatcgctta caaagattga 300  
 150 agatgttatt agaatggtaa ctgtatcaaag 330  
 153 <210> SEQ ID NO: 5  
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 155 <212> TYPE: PRT  
 156 <213> ORGANISM: Artificial Sequence  
 158 <220> FEATURE:  
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 160 Peptide  
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 164 1  
 167 <210> SEQ ID NO: 6  
 168 <211> LENGTH: 9  
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 170 <213> ORGANISM: Artificial Sequence  
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PATENT APPLICATION: US/10/620,795A

DATE: 07/19/2006

TIME: 09:21:32

Input Set : F:\UTSK352.APP.txt

Output Set: N:\CRF4\07192006\J620795A.raw

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203 gtcaaccag ct 12  
206 <210> SEQ ID NO: 9  
207 <211> LENGTH: 22  
208 <212> TYPE: DNA  
209 <213> ORGANISM: Artificial Sequence  
211 <220> FEATURE:  
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216 aacagctgaa gagcttggaa tg 22  
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220 <211> LENGTH: 26  
221 <212> TYPE: DNA  
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224 <220> FEATURE:  
225 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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229 cgataatctt actattcaact agtttc 26  
232 <210> SEQ ID NO: 11  
233 <211> LENGTH: 24  
234 <212> TYPE: DNA  
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237 <220> FEATURE:  
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247 <212> TYPE: DNA  
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252 Primer  
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263 <220> FEATURE:  
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273 <212> TYPE: DNA  
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276 <220> FEATURE:  
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278 Primer  
280 <400> SEQUENCE: 14  
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286 <212> TYPE: PRT  
287 <213> ORGANISM: Artificial Sequence  
289 <220> FEATURE:  
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291 Peptide  
293 <400> SEQUENCE: 15  
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304 <213> ORGANISM: Artificial Sequence  
306 <220> FEATURE:  
307 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
308 Peptide  
310 <400> SEQUENCE: 16  
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312 1 5 10 15  
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317 <212> TYPE: PRT  
318 <213> ORGANISM: Artificial Sequence  
320 <220> FEATURE:  
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322 Peptide  
324 <400> SEQUENCE: 17  
325 Ala Pro Ala Gln Gly Gly Ile Ser Ser Pro Ile Asn Val Thr Thr Ala  
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328 Ile Asp Ala Asn  
329 20  
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**VERIFICATION SUMMARY**

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